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RAW SEQUENCE LISTING

DATE: 08/02/2001

PATENT APPLICATION: US/09/912,436

TIME: 10:45:33

Input Set : A:\48929sequence.app

Output Set: N:\CRF3\08022001\I912436.raw

ENTERED

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3 <110> APPLICANT: JELTSCH, Markku M
4     ALITALO, Kari
5     OLOFSSON, Birgitta
6     ERIKSSON, Ulf
8 <120> TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCEREASING THE
9     AMOUNT OF SOLUBLE VEGF-B
11 <130> FILE REFERENCE: 1064-48929PV Markku JELTSCH et al
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/912,436
C--> 14 <141> CURRENT FILING DATE: 2001-07-26
16 <160> NUMBER OF SEQ ID NOS: 17
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 567
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(567)
29 <220> FEATURE:
30 <221> NAME/KEY: mat_peptide
31 <222> LOCATION: (64)..(564)
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36 -20 -15 -10
38 gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac cag 96
39 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
40 -5 -1 1 5 10
42 agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc cag 144
43 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
44 15 20 25
46 ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc gtg 192
47 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
48 30 35 40
50 gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt ggc 240
51 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
52 45 50 55
54 tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac caa 288
55 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
56 60 65 70 75
58 gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg ggg 336
59 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
60 80 85 90
62 gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa aaa 384
63 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
64 95 100 105
66 aag gac agt gct gtg aag cca gac agc ccc agg ccc ctc tgc cca cgc 432

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67 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
68      110      115      120
70 tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc cgc   480
71 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
72      125      130      135
74 tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag ctc   528
75 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
76 140      145      150      155
78 aac cca gac acc tgc agg tgc cgg aag ctg cga agg tga   567
79 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
80      160      165
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84 <211> LENGTH: 188
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
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90  1      5      10      15
92 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
93      20      25      30
95 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
96      35      40      45
98 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
99      50      55      60
101 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
102 65      70      75      80
104 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
105      85      90      95
107 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
108      100      105      110
110 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
111      115      120      125
113 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
114      130      135      140
116 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
117 145      150      155      160
119 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
120      165      170      175
122 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
123      180      185
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127 <211> LENGTH: 624
128 <212> TYPE: DNA
129 <213> ORGANISM: Homo sapiens
131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)..(621)
135 <220> FEATURE:
136 <221> NAME/KEY: mat_peptide

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142 -20 -15 -10
144 gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac cag 96
145 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
146 -5 -1 1 5 10
148 agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc cag 144
149 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
150 15 20 25
152 ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc gtg 192
153 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
154 30 35 40
156 gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt ggc 240
157 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
158 45 50 55
160 tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac caa 288
161 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
162 60 65 70 75
164 gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg ggg 336
165 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
166 80 85 90
168 gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa aaa 384
169 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
170 95 100 105
172 aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac cgt 432
173 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
174 110 115 120
176 ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca ccc 480
177 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
178 125 130 135
180 tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct gcc 528
181 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
182 140 145 150 155
184 cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc gcc 576
185 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
186 160 165 170
188 gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct tag 624
189 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
190 175 180 185
193 <210> SEQ ID NO: 4
194 <211> LENGTH: 207
195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 4
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200 -20 -15 -10
202 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln

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203  -5          -1  1          5          10
205 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
206          15          20          25
208 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
209          30          35          40
211 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
212          45          50          55
214 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
215  60          65          70          75
217 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
218          80          85          90
220 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
221          95          100          105
223 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
224          110          115          120
226 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
227          125          130          135
229 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
230 140          145          150          155
232 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
233          160          165          170
235 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
236          175          180          185
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240 <211> LENGTH: 408
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (1)..(408)
248 <220> FEATURE:
249 <221> NAME/KEY: mat_peptide
250 <222> LOCATION: (64)..(408)
252 <400> SEQUENCE: 5
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255 -20 -15 -10
257 gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac cag 96
258 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
259 -5 -1 1 5 10
261 agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc cag 144
262 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
263 15 20 25
265 ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc gtg 192
266 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
267 30 35 40
269 gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt ggc 240
270 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
271 45 50 55

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273 tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac caa      288
274 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
275 60      65      70      75
277 gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg ggg      336
278 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
279      80      85      90
281 gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa aaa      384
282 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
283      95      100      105
285 aag gac agt gct gtg aag cca gac      408
286 Lys Asp Ser Ala Val Lys Pro Asp
287      110      115
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291 <211> LENGTH: 136
292 <212> TYPE: PRT
293 <213> ORGANISM: Homo sapiens
295 <400> SEQUENCE: 6
296 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
297 -20      -15      -10
299 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
300 -5      -1 1      5      10
302 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
303      15      20      25
305 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
306      30      35      40
308 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
309      45      50      55
311 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
312 60      65      70      75
314 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
315      80      85      90
317 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
318      95      100      105
320 Lys Asp Ser Ala Val Lys Pro Asp
321      110      115
324 <210> SEQ ID NO: 7
325 <211> LENGTH: 5614
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Description of Artificial Sequence:
331 pSecTagA-VEGF-B167-H6
333 <400> SEQUENCE: 7
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336 ccgcatagtt aagccagtat ctgtccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
338 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
340 ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
342 gattattgac tagttattaa tagtaatcaa ttacgggggc attagttcat agcccatata 300
344 tggagttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc 360

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VERIFICATION SUMMARY

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DATE: 08/02/2001

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Input Set : A:\48929sequence.app

Output Set: N:\CRF3\08022001\I912436.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date